



IFWO

**RAW SEQUENCE LISTING**  
**PATENT APPLICATION: US/10/645,085A**

**DATE: 08/25/2004**  
**TIME: 15:36:23**

**Input Set : A:\65678108.txt**  
**Output Set: N:\CRF4\08252004\J645085A.raw**

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3 <110> APPLICANT: FUKUSHIMA, NAOSHI
4     TSUCHIYA, MASAYUKI
5     OH-EDA, MASAYOSHI
6     UNO, SHINSUKE
7     KIKUCHI, YASUFUMI
8     OHTOMO, TOSHIHIKO
10 <120> TITLE OF INVENTION: AGONIST ANTIBODIES
12 <130> FILE REFERENCE: 065678-0108
14 <140> CURRENT APPLICATION NUMBER: 10/645,085A
C--> 15 <141> CURRENT FILING DATE: 2002-10-07
17 <150> PRIOR APPLICATION NUMBER: PCT/JP01/03288
18 <151> PRIOR FILING DATE: 2001-04-17
20 <150> PRIOR APPLICATION NUMBER: PCT/JP01/01912
21 <151> PRIOR FILING DATE: 2001-03-12
23 <150> PRIOR APPLICATION NUMBER: JP 2000-115246
24 <151> PRIOR FILING DATE: 2000-04-17
26 <150> PRIOR APPLICATION NUMBER: JP 2000-321821
27 <151> PRIOR FILING DATE: 2000-10-20
29 <150> PRIOR APPLICATION NUMBER: JP 2000-321822
30 <151> PRIOR FILING DATE: 2000-10-20
32 <160> NUMBER OF SEQ ID NOS: 138
34 <170> SOFTWARE: PatentIn Ver. 3.2
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38 <212> TYPE: DNA
39 <213> ORGANISM: Artificial Sequence
41 <220> FEATURE:
42 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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51 <213> ORGANISM: Artificial Sequence
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61 <211> LENGTH: 28
62 <212> TYPE: DNA
63 <213> ORGANISM: Artificial Sequence
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 78 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer  
 80 <400> SEQUENCE: 4  
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 91 <222> LOCATION: (1)..(393)  
 92 <223> OTHER INFORMATION: pGEM-M1L. 1-57; signal peptide, 58-394; mature peptide  
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 97 1 5 10 15  
 99 tcc agc agt gat gtt gtg atg acc caa act cca ctc tcc ctg cct gtc 96  
 100 Ser Ser Ser Asp Val Val Met Thr Gln Thr Pro Leu Ser Leu Pro Val  
 101 20 25 30  
 103 agt ctt gga gat caa gcc tcc atc tct tgc aga tct agt cag agc ctt 144  
 104 Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys Arg Ser Gln Ser Leu  
 105 35 40 45  
 107 cta cac agt aaa gga aac acc tat tta caa tgg tac cta cag aag cca 192  
 108 Leu His Ser Lys Gly Asn Thr Tyr Leu Gln Trp Tyr Leu Gln Lys Pro  
 109 50 55 60  
 111 ggc cag tct cca aag ctc ctg atc tac aaa gtt tcc aac cga ttt tct 240  
 112 Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys Val Ser Asn Arg Phe Ser  
 113 65 70 75 80  
 115 ggg gtc cca gac agg ttc agt ggc agt gga tca ggg aca gat ttc aca 288  
 116 Gly Val Pro Asp Arg Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr  
 117 85 90 95  
 119 ctc aag atc agc aga gtg gag gct gag gat ctg gga gtt tat ttc tgc 336  
 120 Leu Lys Ile Ser Arg Val Glu Ala Asp Leu Gly Val Tyr Phe Cys  
 121 100 105 110  
 123 tct caa agt aca cat gtt ccg tac acg tcc gga ggg ggg acc aag ctg 384  
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 128 Glu Ile Lys  
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134 <212> TYPE: DNA  
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 138 <221> NAME/KEY: CDS  
 139 <222> LOCATION: (1)..(408)  
 140 <223> OTHER INFORMATION: pGEM-M1H. 1-57; signal peptide, 58-408; mature peptide  
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145       1                   5                   10                   15	
147 gtc cac tcc cag gtc cag ctg cag cag tct gga cct gac ctg gta aag	96
148 Val His Ser Gln Val Gln Leu Gln Gln Ser Gly Pro Asp Leu Val Lys	
149       20               25                   30	
151 cct ggg gct tca gtg aag atg tcc tgc aag gct tct gga tac acc ttc	144
152 Pro Gly Ala Ser Val Lys Met Ser Cys Lys Ala Ser Gly Tyr Thr Phe	
153       35               40                   45	
155 gtt aac cat gtt atg cac tgg gtg aag cag aag cca ggg cag ggc ctt	192
156 Val Asn His Val Met His Trp Val Lys Gln Lys Pro Gly Gln Gly Leu	
157       50               55                   60	
159 gag tgg att gga tat att tat cct tac aat gat ggt act aag tac aat	240
160 Glu Trp Ile Gly Tyr Ile Tyr Pro Tyr Asn Asp Gly Thr Lys Tyr Asn	
161       65               70                   75                   80	
163 gag aag ttc aag ggc aag gcc aca ctg act tca gag aaa tcc tcc agc	288
164 Glu Lys Phe Lys Gly Lys Ala Thr Leu Thr Ser Glu Lys Ser Ser Ser	
165       85               90                   95	
167 gca gcc tac atg gag ctc agc agc ctg gcc tct gag gac tct gcg gtc	336
168 Ala Ala Tyr Met Glu Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val	
169       100              105                   110	
171 tac tac tgt gca aga ggg ggt tac tat agt tac gac gac tgg ggc caa	384
172 Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Ser Tyr Asp Asp Trp Gly Gln	
173       115              120                   125	
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193       1               5                   10                   15	
195 tcc agc agt gat gtt gtg atg acc caa agt cca ctc tcc ctg cct gtc	96
196 Ser Ser Ser Asp Val Val Met Thr Gln Ser Pro Leu Ser Leu Pro Val	
197       20               25                   30	

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199	agt	ctt	gga	aat	caa	gcc	tcc	atc	tct	tgc	aga	tca	agt	cag	agc	ctt		144
200	Ser	Leu	Gly	Asp	Gln	Ala	Ser	Ile	Ser	Cys	Arg	Ser	Ser	Gln	Ser	Leu		
201		35						40						45				
203	gtg	cac	agt	aat	gga	aag	acc	tat	tta	cat	tgg	tac	ctg	cag	aag	cca		192
204	Val	His	Ser	Asn	Gly	Lys	Thr	Tyr	Leu	His	Trp	Tyr	Leu	Gln	Lys	Pro		
205		50						55						60				
207	ggc	cag	tct	cca	aaa	ctc	ctg	atc	tac	aaa	gtt	tcc	aac	cga	ttt	tct		240
208	Gly	Gln	Ser	Pro	Lys	Leu	Leu	Ile	Tyr	Lys	Val	Ser	Asn	Arg	Phe	Ser		
209		65						70			75			80				
211	ggg	gtc	cca	gac	agg	ttc	agt	ggc	agt	gga	tca	gtg	aca	gat	ttc	aca		288
212	Gly	Val	Pro	Asp	Arg	Phe	Ser	Gly	Ser	Gly	Ser	Val	Thr	Asp	Phe	Thr		
213								85			90			95				
215	ctc	atg	atc	agc	aga	gtg	gag	gct	gag	gat	ctg	gga	gtt	tat	ttc	tgc		336
216	Leu	Met	Ile	Ser	Arg	Val	Glu	Ala	Glu	Asp	Leu	Gly	Val	Tyr	Phe	Cys		
217		100						105						110				
219	tct	caa	agt	aca	cat	gtt	ccg	tac	acg	ttc	gga	ggg	ggg	acc	aag	ctg		384
220	Ser	Gln	Ser	Thr	His	Val	Pro	Tyr	Thr	Phe	Gly	Gly	Gly	Thr	Lys	Leu		
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234	<221>	NAME/KEY:	CDS															
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236	<223>	OTHER INFORMATION:	pGEM-M2H.	1-57;	signal	peptide,	58-408;	mature	peptide									
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241		1				5				10				15				
243	gtc	cac	tcc	cag	gtc	cag	ctg	cag	cag	tct	gga	cct	gaa	ctg	gta	aag		96
244	Val	His	Ser	Gln	Val	Gln	Leu	Gln	Gln	Ser	Gly	Pro	Glu	Leu	Val	Lys		
245						20			25					30				
247	cct	ggg	gct	tca	gtg	aag	atg	tcc	tgc	aag	gct	tct	gga	tac	acc	ttc		144
248	Pro	Gly	Ala	Ser	Val	Lys	Met	Ser	Cys	Lys	Ala	Ser	Gly	Tyr	Thr	Phe		
249						35			40					45				
251	gct	aac	cat	gtt	att	cac	tgg	gtg	aag	cag	aag	cca	ggg	cag	ggc	ctt		192
252	Ala	Asn	His	Val	Ile	His	Trp	Val	Lys	Gln	Lys	Pro	Gly	Gln	Gly	Leu		
253						50			55					60				
255	gag	tgg	att	gga	tat	att	tat	cct	tac	aat	gat	ggt	act	aag	tat	aat		240
256	Glu	Trp	Ile	Gly	Tyr	Ile	Tyr	Pro	Tyr	Asn	Asp	Gly	Thr	Lys	Tyr	Asn		
257						65			70			75		80				
259	gag	aag	ttc	aag	gac	aag	gcc	act	ctg	act	tca	gac	aaa	tcc	tcc	acc		288
260	Glu	Lys	Phe	Lys	Asp	Lys	Ala	Thr	Leu	Thr	Ser	Asp	Lys	Ser	Ser	Thr		
261						85			90					95				
263	aca	gcc	tac	atg	gac	ctc	agc	agc	ctg	gcc	tct	gag	gac	tct	gcg	gtc		336

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264 Thr Ala Tyr Met Asp Leu Ser Ser Leu Ala Ser Glu Asp Ser Ala Val  
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 267 tat tac tgt gca aga ggg ggt tac tat act tac gac gac tgg ggc caa 384  
 268 Tyr Tyr Cys Ala Arg Gly Gly Tyr Tyr Thr Tyr Asp Asp Trp Gly Gln  
 269 115 120 125  
 271 ggc acc act ctc aca gtc tcc tca g 409  
 272 Gly Thr Thr Leu Thr Val Ser Ser  
 273 130 135  
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 325 <211> LENGTH: 30  
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**VERIFICATION SUMMARY** DATE: 08/25/2004  
PATENT APPLICATION: US/10/645,085A TIME: 15:36:25

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